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OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 19:15:11 ; Search time 2887 Seconds  
(without alignments)  
11159.507 Million cell updates/sec

Title: US-09-828-068-1  
Perfect score: 3896  
Sequence: 1 CGCGGCTGTCGGAGCAACG.....gtcaacaccgagaatttac 3896

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 9793542 seqs, 4134689005 residues  
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA\_Main:  
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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	3896	100.0	3896	3	US-09-828-068-1		Sequence 1, Appli
2	3882.4	99.7	4310	6	US-10-447-135-1		Sequence 1, Appli
3	3693.4	94.8	4640	7	US-10-437-963-40889		Sequence 40889, A
4	2952.2	75.8	9455	6	US-10-447-135-3		Sequence 3, Appli
5	173.6	4.5	871	7	US-10-425-114-4042		Sequence 4042, Ap
6	173.6	4.5	884	8	US-10-425-115-140777		Sequence 140777,
7	105.4	2.7	1039	8	US-10-425-115-176502		Sequence 176502,
8	98.8	2.5	835	8	US-10-425-115-128754		Sequence 128754,
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10	73.4	1.9	279	3	US-09-294-093B-2759		Sequence 2759, Ap
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15	43.8	1.1	583	4	US-09-925-065A-549663		Sequence 549663,
16	43.8	1.1	583	4	US-09-925-065A-549664		Sequence 549664,
17	43.8	1.1	583	4	US-09-925-065A-549667		Sequence 549667,
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19	43	1.1	4773	10	US-11-097-143-7462		Sequence 7462, Ap
20	42.2	1.1	319630	7	US-10-398-221-7		Sequence 7, Appli
21	42.2	1.1	3011208	7	US-10-398-221-2058		Sequence 2058, Ap
22	41.8	1.1	610	4	US-09-925-065A-152158		Sequence 152158, Ap
23	41.4	1.1	246	9	US-10-450-763-26483		Sequence 26483, A

ALIGNMENTS

RESULT 1  
US-09-828-068-1  
; Sequence 1, Application US/09828068  
; Patent No. US20020157137A1  
; GENERAL INFORMATION:  
; APPLICANT: Moon, Yong-Hwan  
; APPLICANT: Chen, Lingling  
; APPLICANT: Sung, Zimay R.  
; TITLE OF INVENTION: NUCLEIC ACIDS THAT CONTROL REPRODUCTIVE DEVELOPMENT IN  
; FILE REFERENCE: 018941-001400US  
; CURRENT APPLICATION NUMBER: US/09/828,068  
; CURRENT FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3896  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (241)..(3411)  
US-09-828-068-1

Query Match 100.0%; Score 3896; DB 3; Length 3896;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 1861 TATGTTGTTGAAAGCACAGAAATGGTTCAGAAACATACATGTAATCTCAGCGCAGAGATCAA 1920  
Db 1861 TATGTTGTTGAAAGCACAGAAATGGTTCAGAAACATACATGTAATCTCAGCGCAGAGATCAA 1920  
Qy 1921 TGCCAGATGGAACCGAAAACTCTGTTCTGAGTCACTCGGCAAAAGTTTCTCCAGCTGAG 1980  
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Db 1981 CATGATATCCAAATTTATGTTCTGACCTTCATGAGCAGAGTCTACCCAAAGAAAAAAGAG 2040  
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Db 2161 GACATCAACCGTATTCAATCCAAAGCAACTGCTGATGATGATGATGATGATGATGATGATGAT 2220  
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Qy 2281 GCATCCCAAGTACACAGAGGAGTTACAGGCTCATTTGGCATTTGACCAACAGAGTCT 2340  
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Db	1186	CTTCAGAAAGAGATCCAAAATCTGCTCTCTATCTCGGATTTTCCATGACCGAGAAAAA	1245
Qy	502	TGTGATGAACACAAAGCTAGTTCAAGCCATTTTCTGTAGCAAAAGTTTCCAGCATGGAT	561
Db	1246	TGTGATGNAACAAGAGTAGTTCAAGCCATTTTCTGTAGCAAAAGTTTCCAGCATGGAT	1305
Qy	562	TGCTCGAAGTCTTTGGATAAGTTGAAACTTTAGATAATGGAACAGCACCAAGAACTCTTT	621
Db	1306	TGCTCGAAGTCTTTGGATAAGTTGAAACTTTAGATAATGGAACAGCACCAAGAACTCTTT	1365
Qy	622	CCCGAAGCAGAAATGGCAGAAAGTGTGTTGCTCCATCACAATTTGTTGCGAGCACTTTT	681
Db	1366	CCCGAAGCAGAAATGGCAGAAAGTGTGTTGCTCCATCACAATTTGTTGCGAGCACTTTT	1425
Qy	682	GTGCTGTAGTGTGTTGTTCCAAAAGTGTCTCTAGCACACAATCATCTCAAGGGAAG	741
Db	1426	GTGCTGTAGTGTGTTGTTCCAAAAGTGTCTCTAGCACACAATCATCTCAAGGGAAG	1485
Qy	742	AATGCTGATAGATCAAACTCTTTCCAAAAGTGTGCAAGAGCAATGATCCAAATGCAT	801
Db	1486	AATGCTGATAGATCAAACTCTTTCCAAAAGTGTGCAAGAGCAATGATCCAAATGCAT	1545
Qy	802	CGCCTTCTGCAAGAAATGGAGCTGCTGAGGCCAATCTGATTCACCAATCAAGATTG	861
Db	1546	CGCCTTCTGCAAGAAATGGAGCTGCTGAGGCCAATCTGATTCACCAATCAAGATTG	1605
Qy	862	CAAGGGCCAGCCAAAATATGATGTGGCAGCAAAATGTCTCTGAGGACAAACACTTCTGT	921
Db	1606	CAAGGGCCAGCCAAAATATGATGTGGCAGCAAAATGTCTCTGAGGACAAACACTTCTGT	1665
Qy	922	GATGTTGGGGCTTTACCTGAAGTTCCCGAGATTAATGAGCAATGAGTAAATGGTGCA	981
Db	1666	GATGTTGGGGCTTTACCTGAAGTTCCCGAGATTAATGAGCAATGAGTAAATGGTGCA	1725
Qy	982	GATCAACCTCCATCCACTCCAAAATTTCTGAAGTGTCTCAAGAGAAATGAAGATGAA	1041
Db	1726	GATCAACCTCCATCCACTCCAAAATTTCTGAAGTGTCTCAAGAGAAATGAAGATGAA	1785
Qy	1042	AATGAAAAAATGAAGAGACTCTTGTCTGAGCAGTGCATTTGACCAAAAGATCCTAAC	1101
Db	1786	AATGAAAAAATGAAGAGACTCTTGTCTGAGCAGTGCATTTGACCAAAAGATCCTAAC	1845
Qy	1102	CAATGTCTGNAAGGAAGTATCAGGTTGCTGAGCAGTGCATTTGACCAAAAGATCCG	1161
Db	1846	CCAATGTCTGNAAGGAAGTATCAGGTTGCTGAGCAGTGCATTTGACCAAAAGATCCG	1905
Qy	1162	AAACAGTGTCTGGGCAGAAATGTGACAGATCTGCAATGAGCCATGTGAAGAGTTGTT	1221
Db	1906	AAACAGTGTCTGGGCAGAAATGTGACAGATCTGCAATGAGCCATGTGAAGAGTTGTT	1965
Qy	1222	CTCAAAAGAGCTCCAAATCTAAGAGGAAGACGGATAAGAGTTGATGAAGAGCAGCAG	1281
Db	1966	CTCAAAAGAGCTCCAAATCTAAGAGGAAGACGGATAAGAGTTGATGAAGAGCAGCAG	2025
Qy	1282	CACAGCAAGAAACGACTGCCAGCTGATGTTTTCAGATGCAAAAGCTTTGTCGGAGAAAG	1341
Db	2026	CACAGCAAGAAACGACTGCCAGCTGATGTTTTCAGATGCAAAAGCTTTGTCGGAGAAAG	2085
Qy	1342	CCAAAAAGGTGCGGCTCTATCAGAAATATATAATGCTTAACAGGTTGAGGATCTAGA	1401
Db	2086	CCAAAAAGGTGCGGCTCTATCAGAAATATATAATGCTTAACAGGTTGAGGATCTAGA	2145
Qy	1402	AGTGACGAAGTTTCATGCTGAAATGCGCTGATCCCTGTGAGAGATGATGAAGTCCATC	1461
Db	2146	AGTGACGAAGTTTCATGCTGAAATGCGCTGATCCCTGTGAGAGATGATGAAGTCCATC	2205
Qy	1462	CCGGTCCCATCGAATGAGTATGATTTCTGTTAGCAACATACAGTGGGAGAGAT	1521
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Db	2266	GGGTTAAAAATCAAGTAAGAACAAAGACAAACCGCAAAATCTCTGATGTTGATGATGGA	2325

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Db	2386	GTTGCTCATCCAGCTGGGAATTTTGAGCAACAAAAAAGTGACACCCTCGCGAGTACTCAG	2445
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Db	2446	CATGATGATGAGAAATGATCTGAAAAATGGTCTTGACACAAATATGCAATAGACAGATGTC	2505
Qy	1762	TGTGAGATGATCAGAAATCTCCACAGAGGTGCTCATCAAGGGGAAACAGCGGGT	1821
Db	2506	TGTGAGATGATCAGAAATCTCCACAGAGGTGCTCATCAAGGGGAAACAGCGGGT	2565
Qy	1822	TTGAGTAAGGGGAAAAACACATTCAGCTAGTACCAAAATATGCTGGTGAAGCACACAGA	1881
Db	2566	TTGAGTAAGGGGAAAAACACATTCAGCTAGTACCAAAATATGCTGGTGAAGCACACAGA	2625
Qy	1882	AATGGTCAGAACATACATGATCTCAGCGCAGAAAGATCAATGCCAGATGGAACCGAAAAAC	1941
Db	2626	AATGGTCAGAACATACATGATCTCAGCGCAGAAAGATCAATGCCAGATGGAACCGAAAAAC	2685
Qy	1942	TCTGTTCTGAGTCACTCGGCCAAAGTTTCTCCAGCTGAGCATGATATCCAAATTTATGCT	2001
Db	2686	TCTGTTCTGAGTCACTCGGCCAAAGTTTCTCCAGCTGAGCATGATATCCAAATTTATGCT	2745
Qy	2002	GACCTTCATGAGCAGAGTCTACCCAGAAAGAAAAAGAACAAACTTTGAAGTGACTCGT	2061
Db	2746	GACCTTCATGAGCAGAGTCTACCCAGAAAGAAAAAGAACAAACTTTGAAGTGACTCGT	2805
Qy	2062	GAATAACAGACCATATGATGACATCCCATGATATTTGTAACCTGCTAGCTAATAAAC	2121
Db	2806	GAATAACAGACCATATGATGACATCCCATGATATTTGTAACCTGCTAGCTAATAAAC	2865
Qy	2122	CAGCATGAGAGGAGCTTATGACTGAGACTGATTTGTTCTGACATCAACCGTATTCAATCC	2181
Db	2866	CAGCATGAGAGGAGCTTATGACTGAGACTGATTTGTTCTGACATCAACCGTATTCAATCC	2925
Qy	2182	AAGCAACTGCTGATGATGATTTGTAATAGTGTGCTGCAAGGATGGTTTCAGATTATGCA	2241
Db	2926	AAGCAACTGCTGATGATGATTTGTAATAGTGTGCTGCAAGGATGGTTTCAGATTATGCA	2985
Qy	2242	TCAAAGTGTGTTGACACTTAAATCCCAACAGAAAGTCTTTGGCATCCCAAGGTACACAGAAG	2301
Db	2986	TCAAAGTGTGTTGACACTTAAATCCCAACAGAAAGTCTTTGGCATCCCAAGGTACACAGAAG	3045
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Db	3046	GAGTTTACAGGCTCATTTGGCATTCACCAACAGAGTCTCCACATCTCCAGAACTTTTCAG	3105
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Db	3106	TCTACTCAGGAAACAGCAGACACATTTGCGGATGGAAGAAATGGTCACTATTGCTGCAAGC	3165
Qy	2422	TCACCACTATTTTTCATCATGATCAGTATATTGCTGGAAGCACCACCTGAACTATGG	2481
Db	3166	TCACCACTATTTTTCATCATGATCAGTATATTGCTGGAAGCACCACCTGAACTATGG	3225
Qy	2482	GGCCGTGAGGAGCGAAAGCAATTAACGGGCACTTAAGGGCACTTACAGAAATTTCT	2541
Db	3226	GGCCGTGAGGAGCGAAAGCAATTAACGGGCACTTAAAGGCCCACTTACAGAAATTTCT	3285
Qy	2542	CCAGCAGCAACATGTTGGTGTCTCAATTTAGACTCTGGTATCCAAAGCAGTTGACTTTCT	2601
Db	3286	CCAGCAGCAACATGTTGGTGTCTCAATTTAGACTCTGGTATCCAAAGCAGTTGACTTTCT	3345
Qy	2602	ACTCATGTGAGGATCTTCCAGCAATTTATGCACTCGCCACACAGTAATTCGCCACTG	2661
Db	3346	ACTCATGTGAGGATCTTCCAGCAATTTATGCACTCGCCACACAGTAATTCGCCACTG	3405



Qy 2662 GACCGCTATGCTGAAGAGCGGTTAACCCAGGTCCATGCAAGAAATTTTCCAGCAACA 2721  
Db 3406 GACCGCTATGCTGAAGAGCGGTTAACCCAGGTCCATGCAAGAAATTTTCCAGCAACA 3465  
Qy 2722 GCAACCATGGAAGCGAGTAAGTTATGTGATCGGAGAAATGCTGCAAGTAGTCTTGAT 2781  
Db 3466 GCAACCATGGAAGCGAGTAAGTTATGTGATCGGAGAAATGCTGCAAGTAGTCTTGAT 3525  
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Db 3526 CCTAAAGAAATCCATGCGCTGCGACGCACTTCTCGAAGATGATGGATCCATCAACATTAGCA 3585  
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Db 3946 GCAAAATGGAATGCAATTCAGTGGTGTGTTAGTCCAGTCCAGTCCAGTCCAGTCCAGT 4005  
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Qy 3502 GCTTTGCTGGATCTGCTGAAGGCTTCTTGTAAAGTTGTGGATGCCCATTTTCTGGATG 3561  
Db 4246 GCTTTGCTGGATCTGCTGAAGGCTTCTTGTAAAGTTGTGGATGCCCATTTTCTGGATG 4305  
Qy 3562 GAACCTGCCAGACAGTGAAACAGGGCTTTTGCAGAGGTGCAGCATCCGGTTTGTGGTGC 3621  
Db 4306 GAACCTGCCAGACAGTGAAACAGGGCTTTTGCAGAGGTGCAGCATCCGGTTTGTGGTGC 4365  
Qy 3622 AGTCCAGAAACGTCCTGTTTACTTTGTAGTTGTACTCATCTAGTGGCTGTTTGT 3681  
Db 4366 AGTCCAGAAACGTCCTGTTTACTTTGTAGTTGTACTCATCTAGTGGCTGTTTGT 4425  
Qy 3682 ACAAGGAGAAATGTGAACCTTGTGAAAAAATGTCTCCGCCATTTTGTAAATACCAATA 3741  
Db 4426 ACAAGGAGAAATGTGAACCTTGTGAAAAAATGTCTCCGCCATTTTGTAAATACCAATA 4485  
Qy 3742 AGGAGGTTTATAGTTGTGAGCTGTGTGACTGACGGCGAGAAATGGTTTGTGCGGTG 3801

Db 4486 AGGAGGTTTATAGTTGTGAGCTGTGTGACTGACGGCGAGAAATGGTTTGTGCGTG 4545  
Qy 3802 TTAAGGTTGAAACGACTAGCTCTCGTTATCAATGTGTGTAACTTCTAGATTGATGTG 3861  
Db 4546 TTAAGGTTGAAACGACTAGCTCTCGTTATCAATGTGTGTAACTTCTAGATTGATGTG 4605  
Qy 3862 TACTTACTCTTGAAGTCAACACCGGAGAAATTTAC 3896  
Db 4606 TACTTACTCTTGAAGTCAACACCGGAGAAATTTAC 4640

RESULT 4  
US-10-447-135-3  
; Sequence 3, Application US/10447135  
; Publication No. US20030199684A1  
; GENERAL INFORMATION:  
; APPLICANT: Hirochika, Hirohiko  
; APPLICANT: Yamazaki, Muneo  
; APPLICANT: Miyao, Akio  
; TITLE OF INVENTION: A novel gene involved in brassinosteroid responses  
; FILE REFERENCE: WAFP-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/447,135  
; CURRENT FILING DATE: 2003-05-27  
; PRIOR APPLICATION NUMBER: US 09/721,114  
; PRIOR FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: JAPAN 2000-149106  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 9455  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-10-447-135-3

Query Match 75.8%; Score 2952.2; DB 6; Length 9455;  
Best Local Similarity 87.4%; Pred. No. 0;  
Matches 3487; Conservative 0; Mismatches 23; Indels 481; Gaps 4;  
Qy 386 ACGAACGGGACAAACACCAATTCGAGCATTTTCCATAGAGGGTATGTTGCTTCTTC 445  
Db 5447 ATGCATCTTTATTAATGATAATCTTATTTTCTGTACAGAGGGTATGTTGCTTCTTC 5506  
Qy 446 AGAAGAAGGATCCAAATTTCTGCTCTCTATCTCGAATTTTCCATGACCAAGAAAATGTG 505  
Db 5507 AGAAGAAGGATCCAAATTTCTGCTCTCTATCTCGAATTTTCCATGACCAAGAAAATGTG 5566  
Qy 506 ATGAACACAAAGCTAGTTCAGGCCCAATTTTCTGTAGCAAAAGTTTTCGACGATGGATGCT 565  
Db 5567 ATGAACACAAAGCTAGTTCAGGCCCAATTTTCTGTAGCAAAAGTTTTCGACGATGGATGCT 5626  
Qy 566 CGAAGTCTTGGATAGTTGAAAACCTTCAGATAATGGAACAGCACCAAGAACTCTTCCCG 625  
Db 5627 CGAAGTCTTGGATAGTTGAAAACCTTCAGATAATGGAACAGCACCAAGAACTCTTCCCG 5686  
Qy 626 CAAAGCAGAAATGCAACAAAGTGTGCTTCCATCACATTTGTTTCGAGCACATTTTGTGC 685  
Db 5687 CAAAGCAGAAATGCAACAAAGTGTGCTTCCATCACATTTGTTTCGAGCACATTTTGTGC 5746  
Qy 686 CTGCTAGTGTGTTTCCCAAAAAGTGTCTCTTAGCACACAATCATCTCAAGGGAAGAATG 745  
Db 5747 CTGCTAGTGTGTTTCCCAAAAAGTGTCTCTTAGCACACAATCATCTCAAGGGAAGAATG 5806  
Qy 746 CTGATAGTCAACTCTTCCAAAGAGTGTGCAAGAGCAATGACTCCAATGCAATGCCG 805  
Db 5807 CTGATAGTCAACTCTTCCAAAGAGTGTGCAAGAGCAATGACTCCAATGCAATGCCG 5866  
Qy 806 CTCTCGCAAGAAATGAGGCTGTGAGGCCAATGACTGATTCACCAATGAA----- 854  
Db 5867 CTCTCGCAAGAAATGAGGCTGTGAGGCCAATGACTGATTCACCAATGAAATGATGGTAG 5926  
Qy 855 ----- 854





QY 2690 AGTCCATGCAAGAAATTTTCCAGCAAAATAGCAACCATGGAAGCGAGTAAGTTATGTG 2749  
DB 8147 AGTCCATGCAAGAAATTTTCCAGCAAAATAGCAACCATGGAAGCGAGTAAGTTATGTG 8206  
QY 2750 ATCGGAGAAATCTGGCAAGTAGTCTTGTATCTTAAAGAAATCATGCGTCGCAAGCATC 2809  
DB 8207 ATCGGAGAAATCTGGCAAGTAGTCTTGTATCTTAAAGAAATCATGCGTCGCAAGCATC 8266  
QY 2810 TTCTGAGAAATGATGGATCCATCAACATTTAGCAAGCTTTCCCAACTATGGAACCTTCTAGCA 2869  
DB 8267 TTCTGAGAAATGATGGATCCATCAACATTTAGCAAGCTTTCCCAACTATGGAACCTTCTAGCA 8326  
QY 2870 GGAACAGATGGAGTCTCAACTTCTCATAAATTTCTAGTATGACATCAATTCAGTACAAAGGAT 2929  
DB 8327 GGAACAGATGGAGTCTCAACTTCTCATAAATTTCTAGTATGACATCAATTCAGTACAAAGGAT 8386  
QY 2930 CAACACGACATCATATGGCAGTAACCTGATGGAAGAAATGCAATTCGACATTCGAAGACT 2989  
DB 8387 CAACACGACATCATATGGCAGTAACCTGATGGAAGAAATGCAATTCGACATTCGAAGACT 8446  
QY 2990 TATCAGCGCATCAGCTCATGATCTGCACAGACCTTTTACGCCACATCCTCTAGAGTTGGTG 3049  
DB 8447 TATCAGCGCATCAGCTCATGATCTGCACAGACCTTTTACGCCACATCCTCTAGAGTTGGTG 8506  
QY 3050 TGCTTGGCTCCTTGTCTGCAAGAAATTCGAAATCTGGTCCGGAACCTGTGGCACACAAT 3109  
DB 8507 TGCTTGGCTCCTTGTCTGCAAGAAATTCGAAATCTGGTCCGGAACCTGTGGCACACAAT 8566  
QY 3110 CTGGTTATAGTTAGGAGTCTCAACAGGAATCAATCGATCATGATGGAAGAAAGCAAT 3169  
DB 8567 CTGGTTATAGTTAGGAGTCTCAACAGGAATCAATCGATCATGATGGAAGAAAGCAAT 8626  
QY 3170 ATTTTGAAGCCCTGAAATTTCTGGAATGTTTTCAGCAAAATGGAATGCAATTCGAGTTGGGTT 3229  
DB 8627 ATTTTGAAGCCCTGAAATTTCTGGAATGTTTTCAGCAAAATGGAATGCAATTCGAGTTGGGTT 8686  
QY 3230 CTGTTAGTCCAGTGCAGATTTTATTCAGCGAGGAACAGCATAGTCTCAATCTTGGACCA 3289  
DB 8687 CTGTTAGTCCAGTGCAGATTTTATTCAGCGAGGAACAGCATAGTCTCAATCTTGGACCA 8746  
QY 3290 GAGCGAGGTAATAGTTTTCATCCCTTGTGATCGGTTTGTGACAGGATATCTGTATAA 3349  
DB 8747 GAGCGAGGTAATAGTTTTCATCCCTTGTGATCGGTTTGTGACAGGATATCTGTATAA 8806  
QY 3350 CTAAACAGAACCCAGCTGATTTTACTACATCAGTAACGATAACGAGTATATGATTTACC 3409  
DB 8807 CTAAACAGAACCCAGCTGATTTTACTACATCAGTAACGATAACGAGTATATGATTTACC 8866  
QY 3410 GCTGAAGCAGAAAGTGGTGTGCATAATTCCTGAACATTTTCAATCATACATTTTCACTTTT 3469  
DB 8867 GCTGAAGCAGAAAGTGGTGTGCATAATTCCTGAACATTTTCAATCATACATTTTCACTTTT 8926  
QY 3470 ATGGCGCAATATGATCATCTGTAAAGAGGGGCTTGTGGATCTGCTGTA----- 3521  
DB 8927 ATGGCGCAATATGATCATCTGTAAAGAGGGGCTTGTGGATCTGCTGTAAGGTAAGT 8986  
QY 3522 ----- 3521  
DB 8987 TGAACCTTTTCTTCTGCAAGTTTATCAGTTTAAAGAAAGAAATGATTAATCTATGTTAG 9046  
QY 3522 -----AGGCTTCTTGTAGTTGTGATGCCCCCATTTTCTGGATGGGAAC 3565  
DB 9047 CAAGGATGGTTCTTGTGAGGCTTCTTGTAGTTGTGATGCCCCCATTTTCTGGATGGGAAC 9106  
QY 3566 CTGCCAGACAGTGAACAAGGGCTTTGCAAGGTCGACATCCGGTTTGTGTTGTCAGGTC 3625  
DB 9107 CTGCCAGACAGTGAACAAGGGCTTTGCAAGGTCGACATCCGGTTTGTGTTGTCAGGTC 9166  
QY 3626 CAAGAAACGCTCTCTCTTACTTTGTAGTTGTACTCATACTAGTGGCTTGTGTTGACAA 3685  
DB 9167 CAAGAAACGCTCTCTCTTACTTTGTAGTTGTACTCATACTAGTGGCTTGTGTTGACAA 9226

QY 3686 GGAGAAATGTGAACCTTGTGAAAAAATGTCTCCCCATTTTGTAAATACCATAAGGA 3745  
DB 9227 GGAGAAATGTGAACCTTGTG-AAAAAATGTCTCCCCATTTTGTAAATACCATAAGGA 9285  
QY 3746 GGTTTATAGTGTGTGAGCTGTGTGACTGTGACGGCGAGAAATGGTTTTGTGGGTGTAA 3805  
DB 9286 GGTTTATAGTGTGTGAGCTGTGTGACTGTGACGGCGAGAAATGGTTTTGTGGGTGTAA 9345  
QY 3806 GGTTTGAAACGACTAGCTCTCGTTATCAATGTGTGTTAAACTTCTAGATTGATGTGTACC 3865  
DB 9346 GGTTTGAAACGACTAGCTCTCGTTATCAATGTGTGTTAAACTTCTAGATTGATGTGTACC 9405  
QY 3866 TTACTCTTGAAGTCAACACCGGAGAAATTTAC 3896  
DB 9406 TTACTCTTGAAGTCAACACCGGAGAAATTTAC 9436  
RESULT 5  
US-10-425-114-4042  
; Sequence 4042, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 4042  
; LENGTH: 871  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700347436\_PL1  
US-10-425-114-4042

Query Match 4.5%; Score 173.6; DB 7; Length 871;  
Best Local Similarity 65.3%; Pred. No. 3.2e-39;  
Matches 311; Conservative 0; Mismatches 144; Indels 21; Gaps 3;  
QY 2960 ATGGAAGATTCATTTGACATTCGAAGACTTATCATCGGCATCA---GCTGCATGATCTGC 3016  
DB 105 ATGGAAGCCAAACCGCTGACACTGGAAGACTTGTCTCGCGGTCAATTTCCAGCAAGACTTGC 164  
QY 3017 ACAGACCTTTACGCCCCACATCCTAGAGTTGGTGTCTTGGCTCCTTGTGCTGCAAGAGAAA 3076  
DB 165 GCAGGCTTTTACGCCCTTACCCTTCTGTCGGTGTCTCGTTTCATTTGCTGACAGAGAGA 224  
QY 3077 TTGCAAACTGGTCCGAGAACTGTGGCACAATACTCTGGTTATAGTTAGGAGTGTCAACAG 3136  
DB 225 TCGCAAACTGGTCTGGAACTGCGGCGCAGTCTGGGTACAGACTAGGTGATGTTGTAAG 284  
QY 3137 GAATACATCGCATCAGATGAAAGAAAGAAATTTTGAAGCCCTGAATTTCTGGAATGT 3196  
DB 285 GGAACAGGCGCTGTATGCCAACAGAGAGAGAACTACGAGACCTTGA----- 332  
QY 3197 TTTTCAAAAAATGGAATGCAATTCAGTTGGGTTCTGTAGCT-----CCAGTGCAGATT 3250  
DB 333 GCTCGCAGGATGGAACACCTGCACTTGGGTTCTGTAGCTCTGCTGCCAATCTGGAGT 392  
QY 3251 TTTTATCAGGAGGAACAGCATAGCTCAATCTTGGACCGAGGCAAGGGTAAATGGTTC 3310  
DB 393 ACCGGTTCCATGTATGGTACCGGGTCAGCTTTCGACCACTGGCAATGGGAGGACCATTC 452  
QY 3311 ATCCCTTGGATCGGTTTGTGACAGGATATCTGTATTAATACTACAGAAAGCCAGGCTGATT 3370  
DB 453 ATCCGTTGGATAAGCTCGTGAGGAAGGATATCTGTGTACTATACAGAAAGCCAGCGGATT 512

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QY 3371 TTACTCAATCAATGACGATACGAGTATATGATTACCGCTGAAAGCAGAAAGTGG 3426
Db 513 TCACTGTAATAGTGACAGACGAGTACATGAGAACCCCTTTGAAGAGAGAAAGG 568

RESULT 6
US-10-425-115-140777
; Sequence 140777, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 140777
; LENGTH: 884
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_59872C.1
US-10-425-115-140777

Query Match 4.5%; Score 173.6; DB 8; Length 884;
Best Local Similarity 65.3%; Pred. No. 3.3e-39;
Matches 311; Conservative 0; Mismatches 144; Indels 21; Gaps 3;

QY 2960 ATGGAAGATTCATTCGACATTCGAGACTTATCAGCGCATCA---GCTGCATGATCTGC 3016
Db 117 ATGGAAGCAACCGCTGACATCGGAAGACTTGTCTCGCGGTCATTTCCAGCAAGACTTGC 176

QY 3017 ACAGACCTTTACGCCACATCTAGAGTTGGTGTGCTTGGCTCTCTGTCGAGAGGAAA 3076
Db 177 CGAGGCTTTACGCCCTCACCTCGTGTGCGGTGCTCGGTTCAATTGCTGAGCAGGAGA 236

QY 3077 TTGCAAACTGTCGAGAACTGTGCGCACACAATCTGGTTATTAAGTTAGAGTGTCAACAG 3136
Db 237 TCGCAAACTGTCGGAAGCTCGCGCGCAGTCTGGGTACAGACTAGGTGATTTGTAAG 296

QY 3137 GAATACATCCATCAGATGAACAGAGGAAACATTTTGAAGCCCTGAATTTCTGGAATGT 3196
Db 297 GGACAAAGCCGCTGATGCCAACAGCAGAGGAACTACGAGACCTTGA----- 344

QY 3197 TTTACGAAAATGGAATGCATTTGCAAGTTGGGTTCTGTTAGCT-----CCAGTGCAGATT 3250
Db 345 GCTCGCAGGATGGAACACCTCGAGTTGGGTTCTGTTAGCTCTGCTGCCAATCTGGAGT 404

QY 3251 TTTTATCAGCGAGGAACAGCATAGCTCAATCTTTGACACGAGGCAAGGTAATAATGGTTC 3310
Db 405 ACCGGTTTCCATGGTATGATGATGCGGCTTCAGCCAGTGGCAATGGAGGACCATTC 464

QY 3311 ATCCCTTGATCGGTTTGTGACAGAGGATATCTGTATTAACAAAGAACCCAGCTGATT 3370
Db 465 ATCCGTTGATGATGCTGTGAGAGGATATCTGTGTACTAACAGAAACCCAGCCGATT 524

QY 3371 TTACTACATCAGTAACGATACGAGTATATGATTTACCGCTGGAAGCAGAAAGTGG 3426
Db 525 TCACTGTAATTAGTGACAAGAACGAGTACATGAGAACCCTTTGAAAGAGAGAAAGG 580

RESULT 7
US-10-425-115-176502
; Sequence 176502, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 176502
; LENGTH: 1039
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_92562C.1
US-10-425-115-176502

Query Match 2.7%; Score 105.4; DB 8; Length 1039;
Best Local Similarity 52.5%; Pred. No. 3.7e-19;
Matches 606; Conservative 0; Mismatches 421; Indels 128; Gaps 12;

QY 481 ATTTTCATGACCCAGAAAAAATGTGATGAACACAAAGCTAGTTCAAGCCCATTTTCTGTA 540
Db 4 ATTTTCATAAACCCAGCCACAATATATGATGAGCACCA---TGATTGCTCCCGAGTTTGGTG 60

QY 541 GCAAGTTTCGACGATGGGATTCCTCGAAGTGTCTGTAAGTTGAAAACTTCAGATAAT 600
Db 61 TCAAGTATCATCGATGGGATTCCTCAAGATGCTTGAATGATGATGATGATGATGATGAT 120

QY 601 GGAACAGCAC-CAAGAACTCTTCCCGCAAAAGCAGATGGCACAAAGTGTGCTTCAT 659
Db 121 AGGCAACATCGGAAAAATGTTCTATGACGACAGATGAATGAATGATGCTGCTCTAT 180

QY 660 CACATTTGTCGAGACACTTTTGTGCTGTAGTGTGTTGTTCCCAAAAGTGTCTCTAG 719
Db 181 TTCAATTTGTCGGA-----TTTTGCTTAATAGTGTGTTGATTTCCAGAAAGACTGTTTCTTG 234

QY 720 CACA---CAATCATCTCAAGGGAAGATGCTGTAGATCAACTCTTCCAAAGAGTGTGCA 776
Db 235 CACACAGCAATCATCTCAAGGGA-----TGATCGATTGACCTTTTCAAGACTGCCCA 288

QY 777 AGAAGCAATGACTCCAAATGCAATGGCCCTTCTGGCAAGATGGAGTGTGAGGCCAA 836
Db 289 AGAATGCAAT---TCAAAATGCAAT---TCTCTGCGCAACAAAGCAATTACTCGCATGAA 342

QY 837 TACTGATTCACAAATGAAGATTTTGCAGGCGCCAGCCCAAAATATGATGTGGCAGACAA 896
Db 343 TGTTCAGTAGCTGAAGAAAAATGTTCCAGAGGCACTCGTTGATAGCGGGTTCCATCTAT 402

QY 897 TGTCTCTGAGGACAACTCTGTTGATGTTGGGCTTTTACTGAAAGTTCCCGAGATTAC 956
Db 403 AGAAGTTTTCAGGCTCTCCCAATGATTTGATTTGTCAGCAAAACATCTTGAATGCTGT 462

QY 957 ATGGCACATAGAAGTAATGGTGCAGATCAACCTCCATCCACTCCAAACTTTTCTGAAGT 1016
Db 463 CTCGAAGAATGTCCGCGATTTTACCTGATGATGTTGAAGAAAATGGCACACAGAAATCCCA 522

QY 1017 GGTCTCTCAAAAGAAATGAAGTGAATAAATGGAAAACTGAAGAGACTCTTGTGCTGAGCA 1076
Db 523 CAGTCTAAAACCTTGTGTGGCGCCAAA----- 549

QY 1077 GTGCAATTTGACCAAGATCTTAACCCCAATGTTCTGAAAGGACGTTGATCAGTTGCTGA 1136
Db 550 -----TGAGATGAGATAACATAGCTAATGA 576

QY 1137 GCAGTGCATTTGACCAAGATCCGAAACCACTGTCTGGGCGAAGAAATGTGAGCAGATCTG 1196
Db 577 TCACCTCAATGAGCCTTAATGTTGTAAACCACTATCTGGSCACAAAAGCAAAACAAGTCTG 636

QY 1197 CAATGAGCCATGTGAAGAGTTGTTCTCAAAAGAGCTCCAAATCTTAAGAGGAGACGGA 1256
Db 637 CAACATGGGTCCACGCCGAGCATCGTCAAAAAGAAATGTTGAATCTGATGGTAAGA---- 692

QY 1257 TAAGAAAGTTGATGAAGAGCAGCAGCAGCAAGAAACGCACTGCCCCAGGCTGATGTTTC 1316

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; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 2759
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700346612H1
; NAME/KEY: unsure
; LOCATION: 28, 123, 150, 179, 191, 264
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-2759

Query Match      1.9%; Score 73.4; DB 3; Length 279;
Best Local Similarity 71.3%; Pred. No. 3.7e-10;
Matches 122; Conservative 0; Mismatches 45; Indels 4; Gaps 2;

Qy 2360 ATGGAAGATTCCATTGACATTCGAAGACTTATCAAGCATCA---CGTCATGATCTGC 3016
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3017 ACAGACCTTTACGCCACATCCTAGAGTTGGTGTGCTTGGCTCTTGTCTGTCGAGAGGAAA 3076
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 165 GCAGGCTTTACGNCCTCACCTCGANTCGTGTGCTCGGTTCATTGCTGCAGCAGGAGA 224
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3077 TTGCAAACTGTCGGAGAACTGTGGCACAACTCTGGTTATTAAGTTAGGAG 3127
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 225 TCGCAAACTGCTCTGGGAA-TGCGGGCGCAGTCTGGGTANAGACTAGGTG 274
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-10-425-115-137859
; Sequence 137859, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 137859
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_57203C.1
US-10-425-115-137859

Query Match      1.3%; Score 50.6; DB 8; Length 383;
Best Local Similarity 65.5%; Pred. No. 0.0023;
Matches 74; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 2330 CACAAGAGTCTCCATCCTCAGAACTTTTCACTTACTCAGGAAACAGCAGACACATTTGC 2389
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 270 CAAATTTACCTGCTCTTGATGACATTTTGGAGTGTTACCAAGAACAAACAGACACAACTCC 329
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2390 GGATGGAAGAAATGTCATATTGCTGCNAGCTCACCACCTATTTTCACATCAT 2442
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 330 ACAGGGATGAAGGGGTCAACATTGCATGTACCTCGCTATGTTTCACATCAT 382
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-09-925-065A-549666
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; Sequence 549666, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 549666
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-549666

Query Match      1.2%; Score 45.4; DB 4; Length 583;
Best Local Similarity 44.8%; Pred. No. 0.1;
Matches 169; Conservative 1; Mismatches 207; Indels 0; Gaps 0;

Qy 1516 GAAGATGGTTTAAATCAAGTAAGAACACAAACGCAAAATCTCTGATGTTGTAGAT 1575
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1576 GATGGATCATCCTTATGAACTGGCTGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1635
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 139 GAAAAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 198
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1636 CACACAGTTGCTCATTCAGCTGGGAATTTGAGCAACAAAAAAGTGACACCCCTGCCGAT 1695
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 199 GAAAGAAAAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 258
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1696 ACTCAGCATGATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1755
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 259 GAAAAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 318
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1756 GATGCTGCTCAGCATGTATCAGAAATCTCCACACAGAGGTCTCTCATCAAGGGGAAAAA 1815
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 319 GAAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 378
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1816 CGGGTTTGAAGAGGGGAAAAACATTCAGCTGCTAGTACCAATATGTTGGTGAAGGC 1875
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 379 AGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 438
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1876 ACCGAGATGCTCAGAA 1892
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 439 AAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 455
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-925-065A-549666
; Sequence 549666, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 549665
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-549665
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Query Match 1.1%; Score 44.2; DB 4; Length 583;
Best Local Similarity 44.8%; Pred. No. 0.23;
Matches 169; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

QY 1516 GAAGATGGGTAAATCAAGTAAAGAACAAAGCAAAACGCAAAATCTCTGATGTTGTAGAT 1575
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Db 79 GAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 138

QY 1576 GATGGATCATCTATGAACTGGCTGAATGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 1635
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 GAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 198

QY 1636 CACACATCTCTATGAACTGGCTGAATGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 1695
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 199 GAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 258

QY 1696 ACTCAGCATGATGATGAGATGATCTGAAATGCTTGCACACAAATATGCATAAGACA 1755
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Db 259 GAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 318

QY 1756 GATGCTGTGTCAGCATGTATCAGAAATCTCCACACAGAGGTGCTCATCAAGAGGGGAAACA 1815
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 319 GAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 378

QY 1816 GCGGGTTGATGAGGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 1875
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Db 379 AGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 438

QY 1876 ACCAGAAATGGTCAGAA 1892
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Db 439 AAAAGGAAGGAAGGAAG 455
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RESULT 14
US-09-925-065A-549668
; Sequence 549668, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 549668
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; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-549668

Query Match 1.1%; Score 44.2; DB 4; Length 583;
Best Local Similarity 44.8%; Pred. No. 0.23;
Matches 169; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

QY 1516 GAAGATGGGTAAATCAAGTAAAGAACAAAGCAAAACGCAAAATCTCTGATGTTGTAGAT 1575
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79 GAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 138

QY 1576 GATGGATCATCTATGAACTGGCTGAATGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 1635
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 GAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 198

QY 1636 CACACATCTCTATGAACTGGCTGAATGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 1695
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 199 GAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 258

QY 1696 ACTCAGCATGATGATGAGATGATCTGAAATGCTTGCACACAAATATGCATAAGACA 1755
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 259 GAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 318

QY 1756 GATGCTGTGTCAGCATGTATCAGAAATCTCCACACAGAGGTGCTCATCAAGAGGGGAAACA 1815
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 319 GAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 378

QY 1816 GCGGGTTGATGAGGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 1875
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Db 379 AGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 438

QY 1876 ACCAGAAATGGTCAGAA 1892
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Db 439 AAAAGGAAGGAAGGAAG 455
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RESULT 15
US-09-925-065A-549663
; Sequence 549663, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 549663
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-549663
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Query Match 1.1%; Score 43.8; DB 4; Length 583;
Best Local Similarity 44.6%; Pred. No. 0.3;
Matches 168; Conservative 1; Mismatches 208; Indels 0; Gaps 0;

QY 1516 GAAGATGGGTAAATCAAGTAAAGAACAAAGCAAAACGCAAAATCTCTGATGTTGTAGAT 1575
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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Title: US-09-828-068-1  
Perfect score: 3896  
Sequence: 1 cgcggctgcggagcaacg.....gtcaacaccggagaattac 3896.

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
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9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	45.4	1.2	274	3	US-09-313-294A-3959
C 3	45.2	1.2	1141	3	US-09-806-708B-22
C 4	41.4	1.1	1269	3	US-09-134-001C-197
C 5	41.4	1.1	2848	3	US-09-710-279-3560
C 6	40.8	1.0	2167	2	US-08-874-186-40
C 7	40.8	1.0	126982	3	US-09-949-016-16597
C 8	40.6	1.0	297	3	US-09-134-001C-215
C 9	40.6	1.0	5761	3	US-09-799-451-23
C 10	40.4	1.0	685	3	US-09-166-350-9
C 11	40.2	1.0	505	3	US-09-621-976-15639
C 12	39.8	1.0	601	3	US-09-949-016-33921
C 13	39.8	1.0	601	3	US-09-949-016-133049
C 14	39.8	1.0	1446	3	US-09-248-796A-6694
C 15	39.8	1.0	34068	3	US-09-949-016-15489
C 16	39.8	1.0	51711	3	US-09-949-016-12559
C 17	39.6	1.0	3257	3	US-09-710-279-4067
C 18	39.6	1.0	134890	3	US-09-949-016-15602
C 19	39	1.0	832	3	US-09-621-976-2813
C 20	38.8	1.0	1141	3	US-09-806-708B-22
C 21	38.8	1.0	2311	3	US-09-665-479A-19
C 22	38.2	1.0	395	3	US-09-894-844-45
C 23	38.2	1.0	19566	3	US-09-949-016-12096
C 24	38.2	1.0	19567	3	US-09-949-016-14114

Sequence 809, Appl  
Sequence 14, Appl  
Sequence 8976, Ap  
Sequence 60, Appl  
Sequence 26, Appl  
Sequence 19, Appl  
Sequence 535, App  
Sequence 2195, App  
Sequence 1, Appli  
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Sequence 3, Appli  
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Sequence 12648, A  
Sequence 16741, A  
Sequence 765, App  
Sequence 6914, Ap  
Sequence 2, Appli  
Sequence 1, Appli

US-09-540-236-809  
US-09-596-002-14  
US-09-621-976-8976  
US-09-662-254B-60  
US-09-662-254B-26  
US-09-625-188-19  
US-09-221-017B-535  
US-09-328-352-2195  
US-08-700-651-1  
US-08-928-361B-4  
US-09-588-995A-4  
US-08-700-651-2  
US-08-928-361B-3  
US-09-588-995A-3  
US-10-061-943A-2  
US-09-949-016-12648  
US-09-949-016-16741  
US-09-949-002-765  
US-09-489-039A-6914  
US-09-415-946-2  
US-09-415-946-1

ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232.463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935.313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZ9pt-F18





APPLICATION NUMBER: US/08/874,186  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/782,482  
FILING DATE: 10-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Stephen A.  
REGISTRATION NUMBER: 38,609  
REFERENCE/DOCKET NUMBER: 24884-121392-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4848  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2167 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: intron  
LOCATION: 1..247  
FEATURE:  
NAME/KEY: exon  
LOCATION: 248..367  
FEATURE:  
NAME/KEY: intron  
LOCATION: 368..2167  
US-08-874-186-40

Query Match 1.0%; Score 40.8; DB 2; Length 2167;  
Best Local Similarity 54.7%; Pred. No. 0.23; Mismatches 67; Indels 0; Gaps 0;  
Matches 81; Conservative 0;  
Qy 3610 TTTTGTGTTGGCAGTCCAAAGAAAGCTCTCTGTTACTTTTGTAGTTGTACTCATACTAGT 3669  
Db 171 TATTGTATTTCCATTTTAAAGTAAAGGCAAGGTGATATTTAAGATGTATAGAAATAACAGA 230  
Qy 3670 GCGCTGTTGTACAGAGAGAAATGTGAACCTTGTGCAAAAAATGTCCTCCCATTTT 3729  
Db 231 TATTTGTTATTTTATAGGCTGACTGTGGATCTGTATGGAACTCATGTCTACCTCGTTG 290  
Qy 3730 GTAATTACCAATAAGAGCTTTATAGTGT 3757  
Db 291 ATAAAGTTTACAATAATATATATAGTGT 318

RESULT 7  
US-09-949-016-16597  
Sequence 16597, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16597  
LENGTH: 126982  
TYPE: DNA  
ORGANISM: Human

US-09-949-016-16597

Query Match 1.0%; Score 40.8; DB 3; Length 126982;  
Best Local Similarity 54.7%; Pred. No. 4.8;  
Matches 81; Conservative 0; Mismatches 67; Indels 0; Gaps 0;  
Qy 3610 TTTTGTGTTGGCAGTCCAAAGAAAGCTCTCTGTTACTTTGTAGTTGTACTCATACTAGT 3669  
Db 88856 TATTGTATTTCCATTTTAAAGTAAAGCAAGGTGATATTTAAGATGTATAGAAATAACAGA 88915  
Qy 3670 GCGCTGTTGTACAGAGAGAAATGTGAACCTTGTGCAAAAAATGTCCTCCCATTTT 3729  
Db 88916 TATTGTATTTTATAGGCTGACTGTGGATCTGTATGGAATGAGCTCACTACCTCGTTG 88975  
Qy 3730 GTAATTACCAATAAGAGCTTTATAGTGT 3757  
Db 88976 ATAAAGTTTACAATAATATATATAGTGT 89003

RESULT 8

US-09-134-001C-215/c  
Sequence 215, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynh Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 215  
LENGTH: 297  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-215

Query Match 1.0%; Score 40.6; DB 3; Length 297;  
Best Local Similarity 49.8%; Pred. No. 0.061;  
Matches 103; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
Qy 713 CTCCTAGCACACATCATCTCAAGGGAAGAAATGCTGATAGATCAACTCTTCCAAAGAGTG 772  
Db 208 CTATAAGTGAAAAAGCAATCGAACGTAAACAGGAGCGGTGATTACGTTCAATTATAG 149  
Qy 773 TGAAGAAGGCATGACTCCAAATGCAATGCGCTCTTGGCAAGATGGAGCTGCTGAGG 832  
Db 148 AAGAAGCATTTAAATTGACATCATGTATGTATGTACCTTCTTGAAAAATGTAAGTAAAGTAG 89  
Qy 833 CCAATACGTATTCACCAATGAAAGATTGCAAGGCGCCAGCCCAAAATATATGATGTGGCAG 892  
Db 88 TCATTACTGAACAACAATTAATGAGNAATTGAGCTGGAATTATATATGATGATGAAGGA 29  
Qy 893 CAAATGTCTCTGAGGACAAACATTTCTG 919  
Db 28 ATCTAAATTAATAAGAACAAAGACATCTG 2

RESULT 9

US-09-799-451-23  
Sequence 23, Application US/09799451  
Patent No. 6783969  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Goodrich, Ryle  
APPLICANT: Asundi, Vinod  
APPLICANT: Ren, Feiyan  
APPLICANT: Zhang, Jie







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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15489
; LENGTH: 34068
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15489

Query Match      1.0%; Score 39.8; DB 3; Length 34068;
Best Local Similarity 52.8%; Pred. No. 3.7;
Matches 86; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 3568 GCCAGACAGTGAACAAGGGCTTTCGAAGTGCAGCATCCGGTTTTTGTGTTGCCAGTCCA 3627
Db 16851 GGCTGGCAGCCAGCAGGAGCAGGCGCATGAGCAGGAGGCTGCTCATATATGCCAGTAGT 16792

Qy 3628 AGAAACGTCCCTCTGTACTTTGTAGTTGTACTCATAGTGGCTTTGTTGTACAAGG 3687
Db 16791 ATCAATTTCCCTTGTACTCATGATTTTAATTTAAAGTTTTTTTTTTTTTTTAGA 16732

Qy 3688 AGAAATGTGTAACTTGTGTAAGAAAAATGCTCCCCCATTTTG 3730
Db 16731 AATAGGCTCTCACTCTGTTGTACAGGCTGTATTGCCCAGGCTG 16689

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Qy 1756 GATGCTGTCAGCATGTATCAGAAATCTCCACACAGAGGTGCTCATCAAGGGGAAAAACA 1815  
Db 319 GAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAATTAATGAAGAGGGAAGGA 378  
Qy 1816 GCGGGTTTGAGTAAGGGGAAACACATTCAGCTGCTAGTACCAATATGGTGGTGAAGC 1875  
Db 379 AGGAAAGAAAGGGAAGAAAGAAAGAAATTAATGAAGGAGGGAAGAAAGAAAGAAAT 438  
Qy 1876 ACCAGAAATGTCAGAA 1892  
Db 439 AAAAGAAAGAGAAAGAA 455

RESULT 7  
US-09-925-065A-549664  
; Sequence 549664, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 549664  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-549664

Query Match 1.1%; Score 43.8; DB 6; Length 583;  
Best Local Similarity 44.6%; Pred. No. 0.32;  
Matches 168; Conservative 1; Mismatches 208; Indels 0; Gaps 0;  
Qy 1516 GAAGATGGGTTAAATCAAGTAAAGCAAGCAAAACGCAATATCTCTGATGTTGTAGAT 1575  
Db 79 GAAGCAAGGAAAGGAAAGAAAGAAAGAAAGAAAGGAGAGAGAGAGAGAGAGAGAGAA 138  
Qy 1576 GATGATCATCATCTTATGAACTGCTGAATGGAAGAAAGAAAGAAAGAAAGTGTGAT 1635  
Db 139 GAAAGAAAGGAAAGGAAAGAAATTAAGGAAATTAAGAAAGAAAGAAAGGAAATGGAAA 198  
Qy 1636 CACACAGTTGCTATCCAGCTGGGAATTTAGCAACAAAAAGTGACACCCACTCGGAGT 1695  
Db 199 GAAAGAAATTAAGAAAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 258  
Qy 1696 ACTCAGCATGATGAGAAATGATGATACTGTAATAATGGTCTTTGACACAAAATATGCATAAGACA 1755  
Db 259 GAAAGAAATTAAGAAAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 318  
Qy 1756 GATGCTGTCAGCATGTATCAGAAATCTCCACACAGAGGTGCTCATCAAGGGGAAAAACA 1815  
Db 319 GAAGGAAAGAAAGAAAGGAAAGAAAGGAAAGGAAAGAAAGAAATTAATGAAGGAGGAGGA 378  
Qy 1816 GCGGGTTTGAGTAAGGGGAAAAACATTCAGCTGCTAGTACCAATATGGTGGTGAAGC 1875  
Db 379 AGGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 438  
Qy 1876 ACCAGAAATGTCAGAA 1892

Db 439 AAAAGAAAGAGAAAGAA 455  
RESULT 8  
US-09-925-065A-549667  
; Sequence 549667, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 549667  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-549667

Query Match 1.1%; Score 43.8; DB 6; Length 583;  
Best Local Similarity 44.6%; Pred. No. 0.32;  
Matches 168; Conservative 1; Mismatches 208; Indels 0; Gaps 0;  
Qy 1516 GAAGATGGGTTAAATCAAGTAAAGCAAGCAAAACGCAATATCTCTGATGTTGTAGAT 1575  
Db 79 GAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 138  
Qy 1576 GATGATCATCATCTTATGAACTGCTGAATGGAAGAAAGAAAGAAAGTGTGAT 1635  
Db 139 GAAAGAAAGGAAAGGAAAGAAATTAAGGAAATTAAGAAAGAAAGAAAGGAAATGGAAA 198  
Qy 1636 CACACAGTTGCTATCCAGCTGGGAATTTAGCAACAAAAAGTGACACCCACTCGGAGT 1695  
Db 199 GAAAGAAATTAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 258  
Qy 1696 ACTCAGCATGATGAGAAATGATGATACTGTAATAATGGTCTTTGACACAAAATATGCATAAGACA 1755  
Db 259 GAAAGAAATTAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 318  
Qy 1756 GATGCTGTCAGCATGTATCAGAAATCTCCACACAGAGGTGCTCATCAAGGGGAAAAACA 1815  
Db 319 GAAGGAAAGAAAGAAAGGAAAGAAAGGAAAGGAAAGAAATTAATGAAGGAGGAGGA 378  
Qy 1816 GCGGGTTTGAGTAAGGGGAAAAACATTCAGCTGCTAGTACCAATATGGTGGTGAAGC 1875  
Db 379 AGGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 438  
Qy 1876 ACCAGAAATGTCAGAA 1892  
Db 439 AAAAGAAAGAGAAAGAA 455

RESULT 9  
US-09-925-065A-152158/c  
; Sequence 152158, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single



; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.135  
 ; CURRENT APPLICATION NUMBER: US/09/925,065A  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 152158  
 ; LENGTH: 610  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-925-065A-152158

Query Match 1.1%; Score 41.8; DB 6; Length 610;  
 Best Local Similarity 49.3%; Pred. No. 1.1; Mismatches 112; Indels 0; Gaps 0;  
 Matches 109; Conservative 0;  
 ;  
 QY 962 ACATAGAGTAATGGTGCAGATCAACCTCCATCCACTCCAAACTTTCTGAAGTGTCC 1021  
 DB 414 ACATCAATAAAGCTCCAGTTGTTCTTCATTGATGTTGGAGTAGTGAATGTGTC 355  
 .QY 1022 TCAAAAGAAATGAAGATGAATAAGGAAAACTGAAGAGACTCTTTGTTGCTGAGCAGTGA 1081  
 DB 354 TGAATCAAGGTGATTATGACACTAGTGACCAATGAAGATGACATTTGTTAATACTGCAGAAA 295  
 QY 1082 ATTTGACCAAGATCCTAACCCATGCTCGAAGGAACGTGATCAGTTGCTGAGCAGT 1141  
 DB 294 GAGTGCCTATAGACAACATGGTGAATGTCGGATGGTTATTGAAGGACTAGAGCAGT 235  
 QY 1142 GCAATTTGACCAAGATCCGAAACCACTGCTCGGCGAGAAA 1182  
 DB 234 GTGCATTATACAAACAGGAACTGTGTCAGTTTATATA 194

RESULT 10  
 US-09-925-065A-152157/c  
 ; Sequence 152157, Application US/09925065A  
 ; Publication No. US20040181048A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single  
 ; FILE REFERENCE: 108827.135  
 ; Nucleotide Polymorphisms in the Human Genome  
 ; CURRENT APPLICATION NUMBER: US/09/925,065A  
 ; CURRENT FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 152157  
 ; LENGTH: 610  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-925-065A-152157  
 Query Match 1.1%; Score 41.4; DB 6; Length 610;

Best Local Similarity 48.9%; Pred. No. 1.4;  
 Matches 108; Conservative 1; Mismatches 112; Indels 0; Gaps 0;  
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 QY 962 ACATAGAGTAATGGTGCAGATCAACCTCCATCCACTCCAAACTTTCTGAAGTGTCC 1021  
 DB 414 ACATCAATAAAGCTCCAGTTGTTCTTCATTGATGTTGGAGTAGTGAATGTGTC 355  
 QY 1022 TCAAAAGAAATGAAGATGAATAAGGAAAACTGAAGAGACTCTTTGTTGCTGAGCAGTGA 1081  
 DB 354 TGAATCAAGGTGATTATGACACTAGTGACCAATGAAGATGACATTTGTTAATACTGCAGAAA 295  
 QY 1082 ATTTGACCAAGATCCTTAACCCATGCTCGAAGGAACGTGATCAGTTGCTGAGCAGT 1141  
 DB 294 GAGTGCCTATAGACAACATGGTGAATAATGTCGATGGTTTATTGAAGGACTAGAGCAGT 235  
 QY 1142 GCAATTTGACCAAGATCCGAAACCACTGCTCGGCGAGAAA 1182  
 DB 234 GTGCATTATACAAACAGGAACTGTGTCAGTTTATATA 194

RESULT 11  
 US-10-793-626-3560/c  
 ; Sequence 3560, Application US/10793626  
 ; Publication No. US20050255478A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 ; FILE REFERENCE: PUB480US  
 ; CURRENT APPLICATION NUMBER: US/10/793,626  
 ; CURRENT FILING DATE: 2004-03-04  
 ; PRIOR APPLICATION NUMBER: 60/164,258  
 ; PRIOR FILING DATE: 1999-11-09  
 ; NUMBER OF SEQ ID NOS: 4472  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 3560  
 ; LENGTH: 2848  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: nucleic acid sequence  
 ; US-10-793-626-3560

Query Match 1.1%; Score 41.4; DB 8; Length 2848;  
 Best Local Similarity 49.8%; Pred. No. 3.2;  
 Matches 105; Conservative 0; Mismatches 106; Indels 0; Gaps 0;  
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 QY 713 CTCCTAGCACACATCATCTCAAGGGAAGATGCTGATAGATCAACTCTTCCAAAGATG 772  
 DB 2021 CTATAAGTGAATAAGCAATCGAACGTAAACAGGAGCGCGTGGATTCAATTATAG 1962  
 QY 773 TGCAAGAAGCAATGACTCCAAATGCAATGCAATGCGCTTCTGCAAGAATGGAGCTGAGG 832  
 DB 1961 AGAAGCATTAAATTGACATCATGATGATGATGATGATGATGATGATGATGATGATG 1902  
 QY 833 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 892  
 DB 1901 TCATTACTGAACAAACAATTAATGAAGAAATTTGAGCTTGAATTAATGATGATGATG 1842  
 QY 893 CAAATGCTCTCTGAGGACACACTTCTGTTGA 923  
 DB 1841 ATCTAATTAATAAGAACAGACATCTGCTTA 1811

RESULT 12  
 US-10-932-182A-174387/c  
 ; Sequence 174387, Application US/10932182A  
 ; Publication No. US20060046253A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO



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; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 712529
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-712529
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Query Match      1.0%; Score 40; DB 6; Length 634;
Best Local Similarity 54.9%; Pred. No. 3.5;
Matches 79; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 1149 GACCAAGATCCGAAACCAAGTCTCTGGCAGAAATGTGACGAGATCTCAATGAGCCATG 1208
Db 196 GAAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 255

Qy 1209 TGAAGAAGTCTTCTCAAAAGAGCTCCAAATCTAAGAGAGAGAGAGAGAGAGAGAGAG 1268
Db 256 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 315

Qy 1269 GAAGAAGCAGCAGCAGCAAGAA 1292
Db 316 GAAGAAGCAGCAGCAGCAAGAA 339
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Search completed: March 15, 2006, 19:40:57  
Job time : 921 secs

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